



IFWO

RAW SEQUENCE LISTING

DATE: 10/08/2004

PATENT APPLICATION: US/10/727,358

TIME: 15:45:53

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10082004\J727358.raw

3 <110> APPLICANT: Memorial Sloan-Kettering Cancer Center
 4 Kolesnick, Richard N.
 5 Xing, Hong-Mei R.
 7 <120> TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS
 MEDIATED
 8 TUMORIGENESIS
 W--> 9 <130> FILE REFERENCE: 1216-1-006CIP
 11 <140> CURRENT APPLICATION NUMBER: US 10/727,358
 12 <141> CURRENT FILING DATE: 2003-12-03
 14 <150> PRIOR APPLICATION NUMBER: 60/384,228
 15 <151> PRIOR FILING DATE: 2002-05-30
 17 <150> PRIOR APPLICATION NUMBER: 60/460,023
 18 <151> PRIOR FILING DATE: 2003-04-03
 20 <150> PRIOR APPLICATION NUMBER: PCT/US03/16961
 21 <151> PRIOR FILING DATE: 2003-05-29
 23 <160> NUMBER OF SEQ ID NOS: 38
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 120
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <400> SEQUENCE: 1
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 35 gtgtctaacg acctcacaca gcaggagatc cggaccctag aggcaaagct ggtgaaatac 120
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 39 <211> LENGTH: 41
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Homo sapiens
 43 <400> SEQUENCE: 2
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 46 1 5 10 15
 49 Thr Lys Cys Ser Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
 50 20 25 30
 53 Leu Glu Ala Lys Leu Val Lys Tyr Ile
 54 35 40
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 19
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 60 <213> ORGANISM: Homo sapiens
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 63 ggcagtctgc gcgggctgc 19
 66 <210> SEQ ID NO: 4
 67 <211> LENGTH: 18
 68 <212> TYPE: DNA

ENTERED

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69 <213> ORGANISM: Homo sapiens
71 <400> SEQUENCE: 4
72 tcagtgtcta acgacctc                                     18
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 18
77 <212> TYPE: DNA
78 <213> ORGANISM: Homo sapiens
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81 cggaccctag aggcaaag                                     18
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85 <211> LENGTH: 19
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: antisense oligonucleotide
92 <400> SEQUENCE: 6
93 cagcccgcgc agactgccg                                     19
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 18
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: antisense oligonucleotide
104 <400> SEQUENCE: 7
105 gaggtcgtta gacactga                                     18
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109 <211> LENGTH: 16
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111 <213> ORGANISM: Artificial Sequence
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114 <223> OTHER INFORMATION: antisense oligonucleotide
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117 ctttgcctct agggtc                                     16
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121 <211> LENGTH: 873
122 <212> TYPE: PRT
123 <213> ORGANISM: Mus musculus
125 <400> SEQUENCE: 9
127 Met Asp Arg Ala Ala Leu Arg Ala Ala Ala Met Gly Glu Lys Lys Glu
128 1          5          10          15
131 Gly Gly Gly Gly Gly Ala Ala Ala Asp Gly Gly Ala Gly Ala Ala Val
132          20          25          30
135 Ser Arg Ala Leu Gln Gln Cys Gly Gln Leu Gln Lys Leu Ile Asp Ile
136          35          40          45
139 Ser Ile Gly Ser Leu Arg Gly Leu Arg Thr Lys Cys Ser Val Ser Asn
140          50          55          60
143 Asp Leu Thr Gln Gln Glu Ile Arg Thr Leu Glu Ala Lys Leu Val Lys
144 65          70          75          80
147 Tyr Ile Cys Lys Lys Gln Gln Gln Ser Lys Leu Ser Val Thr Pro Ser Asp

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148				85				90				95				
151	Arg	Thr	Ala	Glu	Leu	Asn	Ser	Tyr	Pro	Arg	Phe	Ser	Asp	Trp	Leu	Tyr
152				100				105					110			
155	Ile	Phe	Asn	Val	Arg	Pro	Glu	Val	Val	Gln	Glu	Ile	Pro	Gln	Glu	Leu
156			115					120					125			
159	Thr	Leu	Asp	Ala	Leu	Leu	Glu	Met	Asp	Glu	Ala	Lys	Ala	Lys	Glu	Met
160		130					135					140				
163	Leu	Arg	Arg	Trp	Gly	Ala	Ser	Thr	Glu	Glu	Cys	Ser	Arg	Leu	Gln	Gln
164	145				150					155					160	
167	Ala	Leu	Thr	Cys	Leu	Arg	Lys	Val	Thr	Gly	Leu	Gly	Gly	Glu	His	Lys
168				165					170					175		
171	Met	Asp	Ser	Gly	Trp	Ser	Ser	Thr	Asp	Ala	Arg	Asp	Ser	Ser	Leu	Gly
172				180					185				190			
175	Pro	Pro	Met	Asp	Met	Leu	Ser	Ser	Leu	Gly	Arg	Ala	Gly	Ala	Ser	Thr
176			195					200					205			
179	Gln	Gly	Pro	Arg	Ser	Ile	Ser	Val	Ser	Ala	Leu	Pro	Ala	Ser	Asp	Ser
180		210					215					220				
183	Pro	Val	Pro	Gly	Leu	Ser	Glu	Gly	Leu	Ser	Asp	Ser	Cys	Ile	Pro	Leu
184	225				230					235					240	
187	His	Thr	Ser	Gly	Arg	Leu	Thr	Pro	Arg	Ala	Leu	His	Ser	Phe	Ile	Thr
188				245					250					255		
191	Pro	Pro	Thr	Thr	Pro	Gln	Leu	Arg	Arg	His	Ala	Lys	Leu	Lys	Pro	Pro
192			260					265					270			
195	Arg	Thr	Pro	Pro	Pro	Pro	Ser	Arg	Lys	Val	Phe	Gln	Leu	Leu	Pro	Ser
196			275					280				285				
199	Phe	Pro	Thr	Leu	Thr	Arg	Ser	Lys	Ser	His	Glu	Ser	Gln	Leu	Gly	Asn
200		290					295				300					
203	Arg	Ile	Asp	Asp	Val	Thr	Pro	Met	Lys	Phe	Glu	Leu	Pro	His	Gly	Ser
204	305				310					315					320	
207	Pro	Gln	Leu	Val	Arg	Arg	Asp	Ile	Gly	Leu	Ser	Val	Thr	His	Arg	Phe
208				325					330					335		
211	Ser	Thr	Lys	Ser	Trp	Leu	Ser	Gln	Val	Cys	Asn	Val	Cys	Gln	Lys	Ser
212			340					345					350			
215	Met	Ile	Phe	Gly	Val	Lys	Cys	Lys	His	Cys	Arg	Leu	Lys	Cys	His	Asn
216			355					360					365			
219	Lys	Cys	Thr	Lys	Glu	Ala	Pro	Ala	Cys	Arg	Ile	Thr	Phe	Leu	Pro	Leu
220		370					375					380				
223	Ala	Arg	Leu	Arg	Arg	Thr	Glu	Ser	Val	Pro	Ser	Asp	Ile	Asn	Asn	Pro
224	385				390					395					400	
227	Val	Asp	Arg	Ala	Ala	Glu	Pro	His	Phe	Gly	Thr	Leu	Pro	Lys	Ala	Leu
228				405					410					415		
231	Thr	Lys	Lys	Glu	His	Pro	Pro	Ala	Met	Asn	Leu	Asp	Ser	Ser	Ser	Asn
232			420					425					430			
235	Pro	Ser	Ser	Thr	Thr	Ser	Ser	Thr	Pro	Ser	Ser	Pro	Ala	Pro	Phe	Leu
236			435					440					445			
239	Thr	Ser	Ser	Asn	Pro	Ser	Ser	Ala	Thr	Thr	Pro	Pro	Asn	Pro	Ser	Pro
240		450					455					460				
243	Gly	Gln	Arg	Asp	Ser	Arg	Phe	Ser	Phe	Pro	Asp	Ile	Ser	Ala	Cys	Ser
244	465				470					475				480		

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247 Gln Ala Ala Pro Leu Ser Ser Thr Ala Asp Ser Thr Arg Leu Asp Asp
248                               485                               490                               495
251 Gln Pro Lys Thr Asp Val Leu Gly Val His Glu Ala Glu Ala Glu Glu
252                               500                               505                               510
255 Pro Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Glu Asp Glu Val
256                               515                               520                               525
259 Asp Asp Leu Pro Ser Ser Arg Arg Pro Trp Arg Gly Pro Ile Ser Arg
260                               530                               535                               540
263 Lys Ala Ser Gln Thr Ser Val Tyr Leu Gln Glu Trp Asp Ile Pro Phe
264 545                               550                               555                               560
267 Glu Gln Val Glu Leu Gly Glu Pro Ile Gly Gln Gly Arg Trp Gly Arg
268                               565                               570                               575
271 Val His Arg Gly Arg Trp His Gly Glu Val Ala Ile Arg Leu Leu Glu
272                               580                               585                               590
275 Met Asp Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val
276                               595                               600                               605
279 Met Asn Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly
280                               610                               615                               620
283 Ala Cys Met Asn Pro Pro His Leu Ala Ile Ile Thr Ser Phe Cys Lys
284 625                               630                               635                               640
287 Gly Arg Thr Leu His Ser Phe Val Arg Asp Pro Lys Thr Ser Leu Asp
288                               645                               650                               655
291 Ile Asn Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly
292                               660                               665                               670
295 Tyr Leu His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn
296                               675                               680                               685
299 Val Phe Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe
300                               690                               695                               700
303 Gly Ile Ser Gly Val Val Arg Glu Glu Arg Arg Glu Asn Gln Leu Lys
304 705                               710                               715                               720
307 Leu Ser His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu
308                               725                               730                               735
311 Met Ile Pro Gly Arg Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala
312                               740                               745                               750
315 Asp Val Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp
316                               755                               760                               765
319 Trp Pro Phe Lys His Gln Pro Ala Glu Ala Leu Ile Trp Gln Ile Gly
320                               770                               775                               780
323 Ser Gly Glu Gly Val Arg Arg Val Leu Ala Ser Val Ser Leu Gly Lys
324 785                               790                               795                               800
327 Glu Val Gly Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu
328                               805                               810                               815
331 Arg Pro Ser Phe Ser Leu Leu Met Asp Met Leu Glu Arg Leu Pro Lys
332                               820                               825                               830
335 Leu Asn Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp
336                               835                               840                               845
339 Ile Asn Ser Ser Lys Val Met Pro Arg Phe Glu Arg Phe Gly Leu Gly
340                               850                               855                               860
343 Thr Leu Glu Ser Gly Asn Pro Lys Met

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344 865                               870
347 <210> SEQ ID NO: 10
348 <211> LENGTH: 866
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 10
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355 1                               5                               10                               15
358 Gly Gly Ala Gly Ala Ala Ala Ser Arg Ala Leu Gln Gln Cys Gly Gln
359                               20                               25                               30
362 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
363                               35                               40                               45
366 Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
367                               50                               55                               60
370 Leu Glu Ala Lys Leu Val Arg Tyr Ile Cys Lys Gln Arg Gln Cys Lys
371 65                               70                               75                               80
374 Leu Ser Val Ala Pro Gly Glu Arg Thr Pro Glu Leu Asn Ser Tyr Pro
375                               85                               90                               95
378 Arg Phe Ser Asp Trp Leu Tyr Thr Phe Asn Val Arg Pro Glu Val Val
379                               100                              105                              110
382 Gln Glu Ile Pro Arg Asp Leu Thr Leu Asp Ala Leu Leu Glu Met Asn
383                               115                              120                              125
386 Glu Ala Lys Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp
387                               130                              135                              140
390 Glu Cys Gly Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr
391 145                              150                              155                              160
394 Gly Leu Gly Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp
395                               165                              170                              175
398 Ala Arg Arg Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala
399                               180                              185                              190
402 Ala Ser Leu Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly
403                               195                              200                              205
406 Asn Ser Ala Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala
407                               210                              215                              220
410 Ser Asp Ser Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys
411 225                              230                              235                              240
414 Ile Pro Leu His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser
415                               245                              250                              255
418 Phe Ile Thr Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu
419                               260                              265                              270
422 Lys Pro Pro Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu
423                               275                              280                              285
426 Leu Pro Ser Phe Pro Thr Leu Thr Arg Arg Lys Ser His Glu Ser Gln
427                               290                              295                              300
430 Leu Gly Asn Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser
431 305                              310                              315                              320
434 His Gly Ser Pro Gln Met Val Arg Arg Asp Ile Gly Leu Ser Val Thr
435                               325                              330                              335
438 His Arg Phe Ser Thr Lys Ser Trp Leu Ser Gln Val Cys His Val Cys

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VERIFICATION SUMMARY

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